Please amend page 20, lines 16-30 of the specification as follows:

PCR amplification and sequence analysis - Target sequences were amplified from the extracted genomic DNA of putative events, by *Pwo* or *Taq* polymerase (Boehringer Mannheim, Indianapolis, IN) with 30 cycles of 35 seconds at 95°C, 35 seconds at 60°C, and 35 seconds at 72°C using a MJ thermocycler (MJ Research, Watertown, MA). For the AHAS621 target, primers common to both AHAS108 and AHAS109 were designed with the following sequences: 5'GCAGTGGGACAGGTTCTAT (PHN21971) (SEQ ID NO: 16) and 5'AGTCCTGCCATCACCATCCA (PHN21972) (SEQ ID NO: 17). For the AHAS165 target, the following primers were used: 5'ACCCGCTCCCCCGTCAT (PHN21973) (SEQ ID NO: 18) and 5'ATCTGCTGCTGGATGTCCTTGG (PHN21974) (SEQ ID NO: 19). For the moPAT/GFPm target, primers used were: 5'CGCAACGCCTACGACTGGA (PHN21976) (SEQ ID NO: 20) and 5'TGATGCCGTTCTTCTGCTTGTC (PHN21978) (SEQ ID NO: 21). PCR fragments were purified and either cloned (see below) or directly sequenced in both directions on an ABI 377 automated sequencer.

In the Claims

Please amend the claims as follows:

1. (Amended) A method to inactivate a gene introduced into a genome of a plant cell, said method comprising:

transforming said plant cell with a nucleic acid molecule comprising a promoter operably linked to a nucleotide sequence comprising said gene; and

introducing into said plant cell at least one chimeric oligonucleotide, said chimeric oligonulceotide having at least a first block of RNA residues and a second block of RNA residues, wherein said first and said second blocks of RNA residues are homologous to said nucleic acid molecule and flank a block of DNA residues, said chimeric oligonucleotide being capable of recognizing and implementing a nucleotide conversion in said nucleic acid molecule.

3. (Amended) The method of claim 1, wherein said nucleotide conversion is in the coding region of said gene.

Please add the following new claims:

9. The method of claim 5, wherein said herbicide resistance gene is a 5-enol pyruvylshikimate-3-phosphate synthase gene.

10. The method of claim 5, wherein said herbicide resistance gene is an acetohydroxy acid synthetase gene.

11. The method of claim 9, wherein said chimeric oligonucleotide is selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10.

12. The method of claim 10, wherein said chimeric oligonucleotide is selected from the group consisting of SEQ ID NO: 11, 12, and 13.

13. The method of claim 1, wherein said plant cell is from a monocot.

14. The method of claim 13, wherein said monocot is maize.

15. The method of claim 1, wherein said plant cell is from a dicot.

16. A method to inactivate a gene introduced into a genome of a plant, said method comprising:

transforming said plant with a nucleic acid molecule comprising a promoter operably linked to a nucleotide sequence comprising said gene;

introducing into said plant at least one chimeric oligonucleotide, said chimeric oligonulceotide having at least a first block of RNA residues and a second block of RNA residues, wherein said first and said second blocks of RNA residues are homologous to said nucleic acid molecule and flank a block of DNA residues, said chimeric oligonucleotide being capable of recognizing and implementing a nucleotide conversion in said nucleic acid molecule.

17. The method of claim 16, wherein said nucleotide conversion is in the promoter.

18. The method of claim 16, wherein said nucleotide conversion is in the coding region of said gene.

19. The method of claim 16, wherein the chimeric oligonucleotide introduces a frameshift in the normal reading frame of the gene.

20. The method of claim 16, wherein the chimeric oligonucleotide introduces a premature stop codon in the normal reading frame of the gene.

21. The method of claim 16, wherein said gene is a marker gene.

22. The method of claim 16, wherein said gene is a herbicide resistance gene.

23. The method of claim 22, wherein said herbicide resistance gene is a 5-enol pyruvylshikimate-3-phosphate synthase gene.

24. The method of claim 22, wherein said herbicide resistance gene is an acetohydroxy acid synthetase gene.

25. The method of claim 23, wherein said chimeric oligonucleotide is selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10.

26. The method of claim 25, wherein said chimeric oligonucleotide is selected from the group consisting of SEQ ID NO: 11, 12, and 13.

27. The method of claim 16, wherein said plant is a monocot.

28. The method of claim 27, wherein said monocot is maize.

29. The method of claim 16, wherein said plant is a dicot.

REMARKS

Status of the Claims

Claims 1-8 were rejected. Claims 9-29 have been added. Claims 1-29 are pending in the present application.

Claim 1 has been amended to correct antecedent basis and to more clearly define the invention. Support for these amendments can be found throughout the specification and in the originally filed claims.

Claim 3 has been amended to have proper antecedent basis. Support for this amendment can be found throughout the specification and in the originally filed claims.

Claims 9-15 have been added. Claims 9 and 10 further recite that the herbicide resistance gene is an EPSPS or an AHAS gene, respectively. Support for these claims can be found, for example, on page 9, lines 31-34, Example 1, and Example 2. Claim 11 further recites that the chimeric oligonucleotide is selected from SEQ ID NOS: 1-10. Support for this claim can be found throughout the specification, for example, on pages 4-5, Example 1, and in SEQ ID NOS: 1-10. Claim 12 recites that the chimeric oligonucleotide is selected from SEQ ID NOS: 11 and 12. Support for this claim can be found, for example, on pages 5-6, Example 2, and in SEQ ID